

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 9, 2005, 13:33:45 ; Search time 742.26 Seconds

(without alignments)

3947.771 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 495

Sequence: 1 MKSPVSDIAPSDGEEGSDRT.....LFAKEVONWAISDHQGHRN 495

Scoring table: OLIGO •

Xgapop 60.0 , Xgapext 60.0

Ygapop 60.0 , Ygapext 60.0

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Word size: 1

Total number of hits satisfying chosen parameters:

8776198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

```
-MODEL=frame+frame+P2N,model -DEV=x1h
-Q=/cgn2.1/usptro/spool/us1976615/runat.08072005.175611.23683/app/query.fasta_1.1358
-DB=N Geneseq_16Dec04 -QPTM=fasta -SUPPFIX=oLIGO_rnG -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oLIGO -TRANS=human40.cdi
-LIST=1000 -DOCALIGN=200 -THR SCORE=Quality THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTPUT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=1000000000
-USER=US0976615@CCN -HEAPSIZ=500 -MINLEN=0 -MAXLEN=1000000000
-NO_MMW -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAEEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
```

Database :

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N Geneseq_16Dec04:*
1: geneseqn190as:*
2: geneseqn190as:*
3: geneseqn200as:*
4: geneseqn200as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2004cs:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	495	100.0	2844	3	Aaz50876 Sheep GBS
2	495	100.0	2844	4	Aad10326 Sheep GFO
3	61	12.3	375	5	Aah52158 Human AFP
4	61	12.3	1485	3	Aaz50880 Human/She
5	61	12.3	1488	4	Aai58115 Human pol

6	1651	6	ABL90384	Human pol	
7	61	12.3	ABL54422	Human ova	
8	61	12.3	Aah99626	Human pro	
9	61	12.3	Aah99626	Human tum	
10	61	12.3	ADQ84158	Human AST	
11	61	12.3	Aaf55900	Human AST	
12	61	12.3	Aar50875	Partial h	
13	61	12.3	ACN91332	Breast ca	
14	61	12.3	Aah79234	Human sod	
15	61	12.3	Aak94976	Human full	
16	61	12.3	Adi132035	Full leng	
17	61	12.3	Aaz50879	Full leng	
18	61	12.3	Aaz50879	Marker Ge	
19	61	12.3	ADJ75057	Marker Ge	
20	61	12.3	ADR14586	Human NF-	
21	61	12.3	ADP25216	PRO polyp	
22	61	12.3	ADL32055	Full leng	
23	48	9.7	AAZ30325	Human gro	
24	33	6.7	AAZ30325	Human sig	
25	33	6.7	ADL55800	Human pol	
26	32	6.5	Aak93901	Human cDN	
27	32	6.5	ADL30328	3' end of	
28	32	6.5	Aai59901	Human pol	
29	30	6.1	Aaz50881	Human/She	
30	29	5.9	Ab137731	Human col	
31	29	5.9	Adi138939	Human ova	
32	29	5.9	ADI67304	Human ova	
33	29	5.9	ADI73702	Human ova	
34	29	5.9	ACN87943	Breast ca	
35	29	5.9	AAS66219	DNA encod	
36	29	5.9	ARK92364	Human cDN	
37	29	5.9	ADL28791	5' end of	
38	29	5.9	AAS77186	DNA encod	
39	29	5.9	ACD05897	Novel hum	
40	18	3.6	Aa12435	Human bre	
41	18	3.6	AAL13566	Human bre	
42	18	3.6	ABq97960	Mouse ES	
43	18	3.6	ACN83647	Breast ca	
44	12	2.4	ACH8066	Human gen	
45	12	2.4	ACH67361	Drosophil	
46	12	2.4	ABL03769	Intestina	
47	12	2.4	ADL24752	Human hac	
48	12	2.4	Aav57909	Gene #45	
49	12	2.4	ABN96956	Adf90827	
50	12	2.4	ADF90827	Human hep	
C	51	12	2.4	Ab103768	Drosophil
52	12	2.4	Aav57926	Hereditar	
53	12	2.4	Aav57903	Hereditar	
54	11	2.2	Abx13555	Murine DNP	
55	11	2.2	Adc25330	Rat DNP1	
56	11	2.2	Adc15493	Mouse DNP	
57	11	2.2	Aak52406	Human pol	
58	11	2.2	Abx13553	Human sec	
59	11	2.2	Abv57903	Human DNP	
60	11	2.2	Abx13554	Rat DNP1	
61	11	2.2	Abc25330	Rat DNP1	
62	10	2.0	ADC15491	Rat DNP1	
63	10	2.0	ADP25333	Bacterial	
64	10	2.0	ADP73853	Renal tox	
65	10	2.0	ABL07417	Drosophil	
66	10	2.0	ABL26551	Drosophil	
67	10	2.0	Ab118113	Drosophil	
68	10	2.0	Adb50888	Toxicity-	
69	10	2.0	Adb5128	Bacterial	
70	10	2.0	Abc42420	Toxicity	
71	10	2.0	Abd51130	Bacterial	
C	72	10	2.0	Ab126650	Drosophil
73	10	2.0	Ab107416	Drosophil	
74	10	2.0	Ab118112	Drosophil	
75	10	2.0	Ab26552	Drosophil	
76	9	1.8	Aah79237	Ruman Na	
77	9	1.8	Aaa87459	Rat hepat	
78	9	1.8	Abq85648	Arabidops	

c	79	9	1.8	511	6	ABQ47112	Oligonucleic	Abq39269	Oligonucleic
c	80	9	1.8	511	6	ABQ47113	Oligonucleic	Abq39268	Oligonucleic
c	81	9	1.8	1188	6	ABQ47113	Oligonucleic	Aaf44897	Human bre
c	82	9	1.8	1188	6	1478	3	Abq47113	Oligonucleic
c	83	9	1.8	1701	4	AAC34230	Arabidopsis	Abq50597	Novel can
c	84	9	1.8	1938	4	AAC34230	Arabidopsis	Abq47239	Oligonucleic
c	85	9	1.8	1952	10	AAS61038	Human lim	Abq47238	Oligonucleic
c	86	9	1.8	2031	4	AAD62831	Human for	Aac07097	Human sec
c	87	9	1.8	2174	5	ABL26653	Drosophil	Aaz80186	Human col
c	88	9	1.8	2316	10	ABK52236	cDNA enco	Aac07100	Human sec
c	89	9	1.8	3317	4	ABP59023	Toxicity-	Aca32325	Prokaryot
c	90	9	1.8	5397	5	AAS66000	Abi28771	Abd13245	Pseudomon
c	91	9	1.8	5634	10	ACD19443	cDNA enco	Abq32970	Oligonucleic
c	92	9	1.8	7402	4	ABP59023	Drosophil	Abq32970	Oligonucleic
c	93	9	1.8	7487	5	AAS92457	DNA enco	Ach87521	Human gen
c	94	9	1.8	14800	6	ABL66291	Lung canc	Aai97325	Human neu
c	95	9	1.8	14800	12	ADP13447	Renal cel	Ada30777	DNA encod
c	102	8	1.6	105	2	AAT20739	Human DNA	Abq31613	Oligonucleic
c	103	8	1.6	117	3	AAS94858	Human can	Abq31612	Oligonucleic
c	104	8	1.6	117	6	ADQ97660	Mouse can	Abq31612	Oligonucleic
c	105	8	1.6	117	6	AAC44002	Ovarian C	Abq31612	Oligonucleic
c	106	8	1.6	117	6	AAC59419	Human can	Abq31612	Oligonucleic
c	107	8	1.6	117	10	ABD32694	Human can	Abq31613	Oligonucleic
c	108	8	1.6	144	6	ABP90618	Human Na	Aac99057	Human pan
c	109	8	1.6	168	13	ADR63777	Human gen	Abq41038	Oligonucleic
c	110	8	1.6	302	10	ACN44002	Overian C	Abq41039	Oligonucleic
c	111	8	1.6	302	12	ADQ59419	Human can	Aai67947	Human CCR
c	112	8	1.6	307	4	ADP08855	cDNA enco	Adt43990	Bacterial
c	113	8	1.6	307	5	AARH79233	Human Na	Adt42222	Plant cDN
c	114	8	1.6	321	13	ADR63777	Cotton cd	Ahs2620	S. epider
c	115	8	1.6	336	8	ABX45212	Bovine ES	Aca20567	Brokaryot
c	116	8	1.6	345	5	AAF66458	Novel hum	Aaz41967	Human myo
c	117	8	1.6	368	3	AAC070101	Novel hum	Abd41039	Pseudomon
c	118	8	1.6	383	10	ADP08855	cDNA enco	Acc61925	Gene sequ
c	119	8	1.6	386	6	ABV88859	Human ova	Adk3543	Disease t
c	120	8	1.6	387	6	ABV88917	Human ova	Ahs2620	S. epider
c	121	8	1.6	390	6	ABX45013	Staphyloc	Aca20567	Brokaryot
c	122	8	1.6	404	5	AAF66458	Novel hum	Adt42848	Corn orth
c	123	8	1.6	404	10	ACD97946	Human col	Adt42848	Corn orth
c	124	8	1.6	425	3	ADD33833	Mouse mit	Adt42848	Corn orth
c	125	8	1.6	429	8	ABV88859	Human col	Abn9523	Gene #302
c	126	8	1.6	429	9	ACR19732	Human adu	Abd13820	Human ova
c	127	8	1.6	438	8	ABX44619	Bovine ES	Aai61282	Human pol
c	128	8	1.6	456	3	AAC070104	Human sec	Aca31549	DNA encod
c	129	8	1.6	487	6	ABK62339	Rat sequ	Abd15072	Pseudomon
c	130	8	1.6	487	10	ABD55558	Toxicity-	Aag91199	HMGF 46 k
c	131	8	1.6	487	10	ABX37053	Bovine ES	Abi02015	Drosophil
c	132	8	1.6	487	10	ABT40558	Primary r	Adt42061	Bacterial
c	133	8	1.6	487	12	ADP71655	Toxicity	Aas26516	Human cDN
c	134	8	1.6	499	10	ADF61849	Renal tox	Abx73857	Human nov
c	135	8	1.6	511	6	ABR94941	Human ald	Aas26693	Human cDN
c	136	8	1.6	513	10	AAC07106	Human sec	Abx73434	Human nov
c	137	8	1.6	536	10	ADD10461	Rat TCH17	Adr0077	Human imm
c	138	8	1.6	545	4	AAT18020	Probe #79	Adj5071	Novel NOV
c	139	8	1.6	545	4	ABA62988	Human foe	Aai59496	Human pol
c	140	8	1.6	545	4	AIA43015	Probe #11	Aaa51570	Human TAN
c	141	8	1.6	545	4	ABA30251	Probe #87	Abd13100	Pseudomon
c	142	8	1.6	545	4	AAK37187	Human sec	Abi14989	Drosophil
c	143	8	1.6	545	4	AAK11400	Human bra	Aas89905	DNA encod
c	144	8	1.6	545	4	AB536858	Human liv	Aas79153	DNA encod
c	145	8	1.6	546	4	AAC09173	Human cDN	Ado1411	Mouse TCH
c	146	8	1.6	553	12	AAC07099	Human sec	Abk87049	Human tra
c	147	8	1.6	553	12	ADQ92266	Human aut	Adg88328	Human tra
c	148	8	1.6	585	6	ABQ16892	Oligonucleic	Ad63618	Human ova
c	149	8	1.6	585	6	ABQ16893	Oligonucleic	Add01422	Mouse TCH
c	150	8	1.6	587	4	AAC37568	Human bon	Abn66146	Streptoco
c	151	8	1.6	587	4	AAK11857	Human bra	Aca50501	Prokaryot

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 9, 2005, 13:42:45 ; Search time 6301.53 Seconds

(without alignments)

3806.273 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 495

Sequence: 1 MKSPVSDLAPSDDGEGSDRT.....LFARGEVONWAISDHQGRHN 495

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0

Ygapop 60.0 , Ygapext 60.0

Egapop 6.0 , Egapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 1

Total number of hits satisfying chosen parameters:

9408497

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODEL=frame\_plus\_p2n, model= -DEV=x1h  
-Q=/cgn2.1/USP0 spool/US09776885/runat.08072005.175612.23689/app query.fasta\_1..1358  
-DB=GenEmb1  
-UNITS=bits  
-DOALIGN=N  
-NORM=ext  
-USER=US09776885  
-NO\_MMAP  
-DEV TIMEOUT=120  
-GBEXT=7  
-GBAPEXT=60  
-DELEXT=7

Database : GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_p1:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_stc:\*

12: gb\_sv:\*

13: gb\_un:\*

14: gb\_v1:\*

Score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	495	100.0	2844	4	AP44578	AF244578 Ovis arie
2	495	100.0	2844	6	BD248126	GBS toxin
3	495	100.0	2844	6	AX207626	Sequence
4	62	12.5	233392	2	AC150504	Bos taurus

5	61	12.3	375	6	AM118967	Sequence
6	61	12.3	1485	6	BD248130	GBS toxin
7	61	12.3	1587	9	AK025880	Homo sapi
8	61	12.3	2512	9	AJ138494	Sequence
9	61	12.3	2512	9	AJ387747	Homo sapi
10	61	12.3	2602	6	BD248125	GBS toxin
11	61	12.3	2712	6	CQ783928	Primer fo
12	61	12.3	2712	6	BD127905	Primer fo
13	61	12.3	2712	9	AK075320	Homo sapi
14	61	12.3	2930	6	BD248129	GBS toxin
15	61	12.3	2930	6	AX207624	Sequence
16	61	12.3	2930	9	AF244577	Homo sapi
17	61	12.3	3292	9	BC020961	Homo sapi
18	61	12.3	3329	6	CQ776623	Sequence
19	61	12.3	3362	6	CO412026	Sequence
20	61	9.7	1229	6	AR026921	Homo sapi
21	61	8.7	11202	9	HSU397H3	Human DNA
22	61	8.7	157749	2	AC025535	Homo sapi
23	61	8.7	185711	2	AC150017	Papio anu
24	61	8.7	187017	2	AC150839	Papio anu
25	61	8.5	752	6	CQ720578	Sequence
26	61	7.1	2006	9	AR026921	Human DNA
27	61	6.9	3121	5	AJ719840	Gallus gallus
28	61	6.7	217	6	AR270039	Sequence
29	61	6.7	149597	2	AC034271	Homo sapi
30	61	6.7	194553	2	AC150717	Callithrix jacchus
31	61	6.7	228433	10	AC097073	Rattus norvegicus
32	61	6.5	853	6	CQ782221	Sequence
33	61	6.5	853	6	BD126930	Primer fo
34	61	6.5	3152	10	BC058785	Mus musculus
35	61	6.1	1485	6	BD48131	GBS toxin
36	61	5.9	199	6	AX341073	Sequence
37	61	5.9	494	6	CO405758	Sequence
38	61	5.9	498	6	CQ392975	Sequence
39	61	5.9	498	6	CO399373	Sequence
40	61	5.9	838	6	CQ780684	Sequence
41	61	5.9	838	6	BD125333	Primer fo
42	61	5.9	144738	2	AC112668	Mus musculus
43	61	5.9	137509	5	BX323884	Zebrafish
44	61	5.5	228862	2	CR346110	Danio rerio
45	61	5.1	56641	2	AL138333	Homo sapi
46	61	5.1	187017	2	AC150839	Papio anu
47	61	5.1	188302	2	AC150022	Papio anu
48	61	3.6	251	11	BV198823	sgnm19895
49	18	3.6	264	6	CQ429871	Sequence
50	18	3.6	349	6	CQ429871	Sequence
51	12	2.4	1874	10	BC018306	Mus musculus
52	12	2.4	1939	6	CQ575136	Sequence
53	12	2.4	2085	3	BT010092	Drosophila melanogaster
54	12	2.4	2266	6	AR036570	Sequence
55	12	2.4	2266	6	BD084119	Polymorph
56	12	2.4	2270	6	CQ15838	Sequence
57	12	2.4	2281	9	U90544	Human sodiu
58	12	2.4	2281	9	HSU90544	Human DNA
59	12	2.4	4899	6	CQ575135	Sequence
60	12	2.4	3444	2	AC014246	Drosophila melanogaster
61	12	2.4	136646	9	AL138726	Human DNA
62	12	2.4	137956	2	AC010918	Drosophila melanogaster
63	12	2.4	148975	2	AC012445	Homo sapi
64	12	2.4	167926	3	AC023485	Drosophila melanogaster
65	12	2.4	174157	3	AC023711	Drosophila melanogaster
66	12	2.4	180662	10	AL590388	Mouse DNA
67	12	2.4	209876	2	AL627315	Mouse DNA
68	12	2.4	235033	6	BD084121	Polymorph
69	12	2.4	237326	6	BD084122	Polymorph
70	12	2.4	240774	2	AC130391	Rattus norvegicus
71	12	2.4	246240	6	AR036572	Sequence
72	12	2.4	246240	6	AR036573	Sequence
73	12	2.4	246240	6	AR036574	Sequence
74	12	2.4	246282	9	HSU9128	Human heparin
75	12	2.4	330299	3	AE003491	Drosophila melanogaster
76	11	2.2	838	5	AY559247	Gallus gallus
77	11	2.2	1299	6	CQ725168	Sequence

78	11	AK116431	3	AK116431	Ciona int	c	151	9	1.8	1952	9	AF218942
79	11	BC069629	9	BC069629	Homo sapi	c	152	9	1.8	2031	6	AF225426
80	11	BC069640	9	BC069640	Homo sapi	c	153	9	1.8	2031	6	CQ609462
81	11	BC069646	9	BC069646	Homo sapi	c	154	9	1.8	2229	10	AB025224
82	11	AX709538	6	AX709538	Sequence	c	155	9	1.8	2229	10	Rattus no
83	11	AX743498	6	AX743498	Sequence	c	156	9	1.8	2316	10	AB025223
84	11	AF324864	10	BC038375	Mus muscu	c	157	9	1.8	2491	10	BC003920
85	11	BC038375	10	BC038375	Mus muscu	c	158	9	1.8	2545	10	Bc027240
86	11	AX709532	6	AX709532	Sequence	c	159	9	1.8	2586	10	AF325535
87	11	AX743492	6	AX743492	Sequence	c	160	9	1.8	3021	3	AY119848
88	11	AB032435	9	AB032435	Homo sapi	c	161	9	1.8	3317	6	CG612639
89	11	AX700122	6	AX700122	Sequence	c	162	9	1.8	4348	3	AY195738
90	11	AX709534	6	AX709534	Sequence	c	163	9	1.8	5000	14	AF033994
91	11	AX743494	6	AX743494	Sequence	c	164	9	1.8	5397	9	AB007955
92	11	AF27471235	5	Rattus no		c	165	9	1.8	7402	6	CQ612638
c	93	AC090586	2	AC090586	Homo sapi	c	166	9	1.8	10734	1	CO612638
c	94	AC118880	2	AC118880	Rattus no	c	167	9	1.8	13706	3	U58737
c	95	AC040936	9	AC040936	Homo sapi	c	168	9	1.8	14569	6	HSPL37
c	96	AC119499	2	AC119499	Rattus no	c	169	9	1.8	14626	9	CQ79189
c	97	AC104009	9	AC104009	Homo sapi	c	170	9	1.8	14646	9	AY480048
c	98	AC113306	9	AC113306	Mus muscu	c	171	9	1.8	14675	9	AY480048
c	99	AC016904	2	AC016904	Homo sapi	c	172	9	1.8	14689	9	AY480050
c	100	AC117110	2	AC117110	Rattus no	c	173	9	1.8	14751	9	AY480046
c	101	AC145086	2	AC145086		c	174	9	1.8	14755	9	AY480044
c	102	AY102171	10	AY102171	Rattus no	c	175	9	1.8	14797	9	AY480051
c	103	AC069459	6	AC069459	Sequence	c	176	9	1.8	14800	6	AX334119
c	104	AC069652	6	AC069652	Sequence	c	177	9	1.8	14800	9	HSU53404
c	105	AX827782	6	AX827782	Sequence	c	178	9	1.8	14835	6	AX281704
c	106	U2438650	2	U2438650	Rattus no	c	179	9	1.8	15249	9	AY480047
c	107	U2438650	10	U2438650	RNA	c	180	9	1.8	20717	2	AC013104
c	108	BT010253	3	BT010253	Drosophil	c	181	9	1.8	22693	9	HSPL37S3
c	109	AY060776	3	AY060776	Drosophil	c	182	9	1.8	37121	3	AC029766
c	110	BC078748	10	BC078748	Rattus no	c	183	9	1.8	38164	2	AC142397
c	111	X77241	5	Mus musculus		c	184	9	1.8	43668	9	AC142398
c	112	BC013445	10	BC013445	Mus muscu	c	185	9	1.8	47337	2	BX548242
c	113	CQ580508	5	CQ580508	Sequence	c	186	9	1.8	64135	9	AL158080
c	114	BT010253	2	BT010253	Drosophil	c	187	9	1.8	74629	9	AC101440
c	115	CQ580607	6	CQ580607	Sequence	c	188	9	1.8	75001	9	AC093167
c	116	CQ586551	6	CQ586551	Sequence	c	189	9	1.8	76813	9	AL646016
c	117	BT010254	10	BT010254	Mus muscu	c	190	9	1.8	78340	5	AL935228
c	118	BT010254	10	BT010254	Mus muscu	c	191	9	1.8	86710	5	ATF23E12
c	119	CET07A5	6	CET07A5	Sequence	c	192	9	1.8	86998	9	AP006275
c	120	AC020252	2	AC020252	Drosophil	c	193	9	1.8	101601	9	AC079334
c	121	AC094088	9	AC094088	Homo sapi	c	194	9	1.8	107893	5	BX276180
c	122	AC044345	3	AC044345	Drosophil	c	195	9	1.8	109138	9	AC104084
c	123	AC080597	9	AC080597	Homo sapi	c	196	9	1.8	110000	1	REUB0228_0
c	124	BX321891	2	BX321891	Danio rer	c	197	9	1.8	117218	2	AC110229_0
c	125	Contamination	3	Contamination	(3 of	c	198	9	1.8	117282	2	AL359229
c	126	AC018326	5	AC018326	Drosophil	c	199	9	1.8	119199	2	AC03812
c	127	BX294657	5	BX294657	Zebrafish	c	200	9	1.8	127274	10	AL932270
c	128	AC034271	2	AC034271	Homo sapi	c	201	9	1.8	135620	9	AC146048
c	129	AC023952	2	AC023952	Drosophil	c	202	9	1.8	137218	2	OSJN0037
c	130	AC077556	3	AC077556	Drosophil	c	203	9	1.8	138780	8	AP004344
c	131	AC077557	3	AC077557	Drosophil	c	204	9	1.8	140489	2	AC02306
c	132	AC099016	3	AC099016	Drosophil	c	205	9	1.8	142726	8	AP003112
c	133	AC121663	2	AC121663	Rattus no	c	206	9	1.8	150856	9	AC087072
c	134	AL606464	10	AL606464	Mouse DNA	c	207	9	1.8	15448	2	AC074261
c	135	AL627315	2	AL627315	Drosophil	c	208	9	1.8	153353	4	AC150107
c	136	AE003730	3	AE003730	Drosophil	c	209	9	1.8	155643	8	AP000391
c	137	AE003731	2	AE003731	Drosophil	c	210	9	1.8	156064	9	AC083864
c	138	AE003798	10	AE003798	Drosophil	c	211	9	1.8	156772	8	AC073405
c	139	P2617628	9	P2617628	09	c	212	9	1.8	157848	8	AP005744
c	140	HVLP90	8	HVLP90		c	213	9	1.8	158810	8	AP006266
c	141	AC099028	3	AC099028	Drosophil	c	214	9	1.8	162198	8	AP005916
c	142	AX062556	6	AX062556	Sequence	c	215	9	1.8	163028	9	AC005877
c	143	AY133542	8	AY133542	Arabidops	c	216	9	1.8	164511	2	AC122778
c	144	AF462834	8	AF462834	Arabidops	c	217	9	1.8	165041	8	AP005837
c	145	AY089078	8	AY089078	Arabidops	c	218	9	1.8	165269	9	AC140551
c	146	AF326358	10	AF326358	Mus muscu	c	219	9	1.8	167161	2	AL645945
c	147	BC014364	9	BC014364	Homo sapi	c	220	9	1.8	167578	5	BX649370
c	148	AC093854	10	AC093854	Homo sapi	c	221	9	1.8	167663	9	AC093854
c	149	AL645630	9	AL645630	Mouse DNA	c	222	9	1.8	167898	10	AL645630
c	150	AL161910	9	AL161910	Human DNA	c	223	9	1.8	171025	9	AL161910

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 9, 2005, 16:46:21 ; Search time 4969.57 Seconds  
(without alignments)

4105.478 Million cell updates/sec

Title: US-09-776-865-2

Perfect score: 536

Sequence: 1 MAAGAMTPRPRVQjAPRGFF.....LFAKGEVQNWALNDHGHGRH 536

Scoring table: OLIIGO

Xgapext	60.0	Xgapext	60.0
Ygapext	60.0	Ygapext	60.0
Fgapext	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 1

Total number of hits satisfying chosen parameters: 68477535

Minimum DB Seq length: 0

Maximum DB Seq length: 20000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

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-DB=EST -QMT=SFASTAP -SUFFIX=oligo rst -MINMATCH=0.1 -LGOPCH=0 -LGOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo.cdi -LIST=1000
-DOCAIGN=0 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFORMAT=pfo
-NORM=ext -HEAPSIZE=-500 -MINLEN=0 -MAXLEN=20000000000
-USERFILE=US09776865@CGN 1.1_6461 @runat_08072005_175612_23695 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORE=0.0 -WAIT -DSPLOC=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=60 -XGAPEXT=60 -FGAPPOP=6
-FGAPEXT=7 -YGAPOP=60 -DELPOP=6 -YGAPEXT=60 -DELEXT=7
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Database : EST:\*

1: gb_est1:*
2: gb_est2:*
3: gb_hrc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gbs1:*
9: gb_gbs2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	520	97.0	3189	3	CR618872	CR618872 Full-length
2	285	53.2	1038	5	BY439809	BY439809 BX439809
3	251	46.8	1051	1	AL550137	AL550137 BX439812
4	211	39.4	663	7	CY023522	CY023522 BX439813
5	201	37.5	605	7	BX479639	BX479639 BX479639
6	194	36.2	584	5	DKPZP88F	DKPZP88F BX479640
7	194	36.2	913	5	BX348297	BX348297 BX348297
8	193	36.0	581	5	BP298092	BP298092 BP298092
9	35.8	582	5	BP302998	BP302998 BP302998	

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	520	97.0	3189	3	CR618872	CR618872 Full-length
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4	211	39.4	663	7	CY023522	CY023522 BX439813
5	201	37.5	605	7	BX479639	BX479639 BX479639
6	194	36.2	584	5	DKPZP88F	DKPZP88F BX479640
7	194	36.2	913	5	BX348297	BX348297 BX348297
8	193	36.0	581	5	BP298092	BP298092 BP298092
9	35.8	582	5	BP302998	BP302998 BP302998	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	520	97.0	3189	3	CR618872	CR618872 Full-length
2	285	53.2	1038	5	BY439809	BY439809 BX439809
3	251	46.8	1051	1	AL550137	AL550137 BX439812
4	211	39.4	663	7	CY023522	CY023522 BX439813
5	201	37.5	605	7	BX479639	BX479639 BX479639
6	194	36.2	584	5	DKPZP88F	DKPZP88F BX479640
7	194	36.2	913	5	BX348297	BX348297 BX348297
8	193	36.0	581	5	BP298092	BP298092 BP298092
9	35.8	582	5	BP302998	BP302998 BP302998	

B1851890	6.0	658	4	B1851890	60378047	156	16	3.0	344	5	BY021590	
CB311739	6.0	32	83	CB311739	AGENCOURT	c	157	16	3.0	423	9	CG653532
BU04522	6.0	1240	5	BU04522	AGENCOURT	c	158	16	3.0	909	9	CNS03M9J
CB713294	5.8	32	84	CB713294	AMGNNUC:C	c	159	16	3.0	1024	9	CNS03MJZ
BB537525	5.8	90	85	BB537525	BB537525	c	160	15	2.8	228	6	CD730851
AK087395	5.8	31	86	AK087395	MUS muscu	c	161	15	2.8	239	5	BY179630
AW513337	5.6	321	87	AW513337	UI-R-C4-a	c	162	15	2.8	239	5	CB760265
CR775730	5.4	29	88	CR775730	DKFD469C	c	163	15	2.8	485	4	BI041275
BJ520485	5.0	91	89	BJ520485	BJ520485	c	164	15	2.8	560	4	BJ032567
AJ734277	5.0	27	90	AJ734277	AJ734277	c	165	15	2.8	575	4	BJ692156
BG400668	5.0	92	91	BG400668	602643341	c	166	15	2.8	603	4	BJ703130
BB613552	5.0	27	93	BB613552	BB613552	c	167	15	2.8	647	4	BI445333
BX882862	5.0	94	94	BX882862	BX882862	c	168	14	2.8	647	4	BY645660
BG290613	5.6	30	89	BG290613	6023888889	c	169	14	2.6	412	6	BY645660
AL792191	5.0	95	96	AL792191	AL792191	c	170	14	2.6	604	1	BI041275
CF285351	4.9	27	97	CF285351	AGENCOURT	c	171	13	2.4	2674	3	AK014522
CB747168	4.7	25	98	CB747168	AMGNNUC:C	c	172	13	2.4	563	7	CK876614
CB747168	4.7	25	99	CB747168	AMGNNUC:C	c	173	13	2.4	596	6	ssalpinb5
CB728076	4.5	24	100	CB728076	AMGNNUC:C	c	174	13	2.4	646	9	DR48DT
CR045573	4.5	24	101	CR045573	Forward:c	c	175	13	2.4	687	5	BX864265
BU692199	4.5	24	102	BU692199	BU692199	c	176	12	2.2	943	9	CNS052ZN
BP539146	4.5	24	103	BP539146	6020533009	c	177	12	2.2	387	8	AZ772115
CB365128	4.3	23	104	CB365128	ZP011-P00	c	178	12	2.2	668	4	BJ649120
CK687033	4.3	23	105	CK687033	ZP011-P00	c	179	12	2.2	673	4	BJ646218
CB728076	4.3	23	106	CB728076	ZP011-P00	c	180	11	2.1	300	5	BY278427
CR045573	4.3	23	107	CR045573	ZP011-P00	c	181	11	2.1	359	7	R11332
CK696626	4.3	23	108	CK696626	ZP011-P00	c	182	11	2.1	431	7	H52987
CK024678	4.3	23	109	CK024678	AGENCOURT	c	183	11	2.1	472	5	BY240979
CN718455	4.3	23	110	CN718455	AGENCOURT	c	184	11	2.1	485	6	CB727115
CG493267	4.3	23	111	CG493267	OST39440	c	185	11	2.1	548	5	BQ366104
CF417013	4.1	22	112	CF417013	STR01011	c	186	11	2.1	581	5	BP361755
CK690892	4.1	22	113	CK690892	ZF1011-P00	c	187	11	2.1	582	5	BP309703
CK696626	4.1	22	114	CK696626	ZF1011-P00	c	188	11	2.1	596	6	BP38987
BY478871	4.1	22	115	BY478871	AGENCOURT	c	189	11	2.1	604	2	AV964340
AJ447666	4.1	22	116	AJ447666	AJ447666	c	190	11	2.1	605	7	CF534235
AJ455947	4.1	22	117	AJ455947	AJ455947	c	191	11	2.1	615	2	AV963192
BE876444	4.1	22	118	BE876444	601486880	c	192	11	2.1	616	5	AV963492
BY651156	4.1	22	119	BY651156	BY651156	c	193	11	2.1	634	5	BU611955
CB742771	4.1	22	120	CB742771	AMGNNUC:C	c	194	11	2.1	635	6	BY723745
BY478871	4.1	22	121	BY478871	BY478871	c	195	11	2.1	636	4	BU617191
AJ447666	4.1	22	122	AJ447666	AJ447666	c	196	11	2.1	648	5	BU331471
AJ455947	4.1	22	123	AJ455947	AJ455947	c	197	11	2.1	649	5	BW328845
BE876444	4.1	22	124	BE876444	601486880	c	198	11	2.1	652	7	CF735479
AJ455169	4.1	22	125	AJ455169	AJ455169	c	199	11	2.1	654	5	BU611275
BY190277	3.9	21	119	BY190277	BY190277	c	200	11	2.1	655	6	BY723745
BY138011	3.9	21	120	BY138011	BY138011	c	201	11	2.1	669	5	BU347197
BY793266	3.9	21	121	BY793266	BY793266	c	202	11	2.1	673	5	BW331471
BY196504	3.9	21	122	BY196504	BY196504	c	203	11	2.1	678	7	CN154791
BY234055	3.9	21	123	BY234055	BY234055	c	204	11	2.1	688	7	CN156898
BY278620	3.9	21	124	BY278620	BY278620	c	205	11	2.1	689	5	BU611275
BY246932	3.9	21	125	BY246932	BY246932	c	206	11	2.1	696	6	CB247147
BY031138	3.9	21	126	BY031138	BY031138	c	207	11	2.1	697	5	BU347197
BY793266	3.9	21	127	BY793266	BY793266	c	208	11	2.1	700	7	BU347197
BY196504	3.9	21	128	BY196504	BY196504	c	209	11	2.1	707	3	CU413667
BY284055	3.9	21	129	BY284055	BB862822	c	210	11	2.1	708	5	BU347197
BY278620	3.9	21	130	BY278620	BY278620	c	211	11	2.1	709	5	BU347197
CG533752	3.9	21	131	CG533752	OST119370	c	212	11	2.1	713	7	CK420161
BB654731	3.9	21	132	BB654731	BB654731	c	213	11	2.1	728	5	BI041275
CR421776	3.9	21	133	CR421776	CR421776	c	214	11	2.1	729	7	CK420266
BF123545	3.9	21	134	BF123545	BF123545	c	215	11	2.1	739	4	AY415644
BU907838	3.9	21	135	BU907838	BU907838	c	216	11	2.1	740	5	BU908615
BB866603	3.9	21	136	BB866603	BB866603	c	217	11	2.1	741	5	BU347197
CG533752	3.9	21	137	CG533752	CG533752	c	218	11	2.1	742	5	BI041275
AJ734268	3.7	20	138	AJ734268	AJ734268	c	219	11	2.1	743	5	CD784886
BE754211	3.7	20	139	BE754211	BE754211	c	220	11	2.1	744	5	CD784886
BP214137	3.7	20	140	BP214137	BP214137	c	221	11	2.1	745	5	CD784886
BF124137	3.7	20	141	BF124137	BF124137	c	222	11	2.1	746	5	CD784886
BP214137	3.7	20	142	BP214137	BP214137	c	223	11	2.1	747	5	CD784886
BP214137	3.7	20	143	BP214137	BP214137	c	224	11	2.1	748	5	CD784886
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BP214137	3.7	20	167	BP214137	BP214137	c	248	11	2.1	772	5	CD784886
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BP214137	3.7	20	169	BP214137	BP214137	c	250	11	2.1	774	5	CD784886
BP214137	3.7	20	170	BP214137	BP214137	c	251	11	2.1	775	5	CD784886
BP214137	3.7	20	171	BP214137	BP214137	c	252	11	2.1	776	5	CD784886
BP214137	3.7	20	172	BP214137	BP214137	c	253	11	2.1	777	5	CD784886
BP214137	3.7	20	173	BP214137	BP214137	c	254	11	2.1	778	5	CD784886
BP214137	3.7	20	174	BP214137	BP214137	c	255	11	2.1	779	5	CD784886
BP214137	3.7	20	175	BP214137	BP214137	c	256	11	2.1	780	5	CD784886
BP214137	3.7	20	176	BP214137	BP214137	c	257	11	2.1	781	5	CD784886
BP214137	3.7	20	177	BP214137	BP214137	c	258	11	2.1	782	5	CD784886
BP214137	3.7	20	178	BP214137	BP214137</td							

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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 9, 2005, 21:49:36 ; Search time 909.796 Seconds  
(without alignments)  
3699.824 Million cell updates/sec

Title: US-09-776-865-2

Perfect score: 536

Sequence: 1 MAAGAMTPDRPVQARPGGF.....LFAKGEVONWALNDHHGHRH 536

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delopt 6.0 , Delext 7.0

Searched: 6330943 seqs, 3139157217 residues

Word size: 1

Total number of hits satisfying chosen parameters: 12650797

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

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-DB=Published_Applications_NA_CEMT-fastP -SUFFIXX=oligo.rnpb -MINMATCH=0.1
-LOOPCL=1 -LOOPEXT=0
-TRANS=human40 .cdi -LIST=1000 -DOALIGN=0.0 -THR SCORE=quality -THR MIN=1
-MAXLEN=2000000000 -USERID=US09776865 @CGN_1.1_1065_@runat_08072005_175614_23755
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-PGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -DELEXT=7
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Database : Published\_Applications\_NA:\*

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5: /cgn2_6/podata[2]/pubna/[US07_NEW_PUB.seq:*
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17: /cgn2_6/podata[2]/pubna/[US10E_PUBCOMB.seq:*
18: /cgn2_6/podata[2]/pubna/[US10F_PUBCOMB.seq:*
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20: /cgn2_6/podata[2]/pubna/[US10I_PUBCOMB.seq:*
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26: /cgn2_6/podata[2]/pubna/[US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	536	100.0	2930	9 US-09-776-865-1	Sequence 1, Appli	
2	536	100.0	2930	21 US-0-123-506-7	Sequence 7, Appli	
3	529	98.7	2626	14 US-0-198-846-12482	Sequence 12482, A	
4	529	98.7	3362	10 US-0-814-353-19097	Sequence 19097, A	
5	522	97.4	3292	21 US-0-108-553-858	Sequence 587, Appli	
6	522	97.4	3329	19 US-0-107-589-587	Sequence 587, Appli	
7	514	95.9	2602	21 US-0-10-823-506-1	Sequence 1, Appli	
8	394	73.5	1488	13 US-10-198-841-322	Sequence 322, App	
9	284	53.0	1872	17 US-10-264-049-302	Sequence 302, App	
10	217	40.5	1651	17 US-10-264-237-946	Sequence 946, App	
11	180	33.6	1975	18 US-10-196-461	Sequence 461, App	
12	162	30.2	494	10 US-0-814-153-12829	Sequence 12829, A	
13	151	28.2	498	10 US-0-814-253-46	Sequence 46, Appli	
14	151	28.2	498	10 US-0-814-553-644	Sequence 644, App	
15	151	28.2	516	14 US-10-198-846-903	Sequence 903, App	
16	119	22.2	1229	18 US-10-641-643	Sequence 660, App	
c	17	109	20.3	1975	18 US-10-296-115-461	Sequence 4797, App
c	18	108	20.1	756	14 US-10-198-846-4777	Sequence 602, App
c	19	69	12.9	217	17 US-10-305-720-602	Sequence 1320, App
c	20	64	11.9	196	9 US-09-818-178-1320	Sequence 1320, App
c	21	64	11.9	196	13 US-10-046-335-1120	Sequence 1320, App
c	22	64	11.9	196	14 US-10-116-50-1320	Sequence 1320, App
c	23	61	11.4	1485	21 US-10-823-506-9	Sequence 9, Appli
c	24	61	11.4	2844	9 US-09-776-865-3	Sequence 3, Appli
c	25	61	11.4	2844	21 US-10-823-506-3	Sequence 3, Appli
c	26	30	1485	21 US-10-823-506-11	Sequence 11, Appli	
c	27	21	3.9	573	9 US-09-728-446-1228	Sequence 1228, App
c	28	11	2.1	1549	11 US-09-968-007A-234	Sequence 234, App
c	29	11	2.1	1549	11 US-09-968-007A-692	Sequence 692, App
c	30	11	2.1	1549	21 US-10-843-641A-6704	Sequence 6704, App
c	31	11	2.1	1549	21 US-10-843-641A-7162	Sequence 7162, App
c	32	11	2.1	2528	20 US-10-134-734-731-13	Sequence 13, Appi
c	33	11	2.1	2528	20 US-10-807-500-13	Sequence 13, Appi
c	34	11	2.1	3423	16 US-10-233-045-21	Sequence 21, Appi
c	35	11	2.1	3946	20 US-10-734-731-9	Sequence 9, Appli
c	36	11	2.1	3946	20 US-10-807-500-9	Sequence 9, Appli
c	37	11	2.1	3946	21 US-10-887-553A-1016	Sequence 1016, App
c	38	11	2.1	3982	18 US-10-205-131-8	Sequence 8, Appli
c	39	11	2.1	3982	20 US-10-734-731-11	Sequence 11, Appli
c	40	11	2.1	3982	20 US-10-807-500-11	Sequence 11, Appli
c	41	10	1.9	512	16 US-10-029-386-556	Sequence 556, App
c	42	10	1.9	657	17 US-10-398-221-2881	Sequence 2581, App
c	43	10	1.9	875	17 US-10-369-493-29558	Sequence 29558, A
c	44	10	1.9	1425	17 US-10-369-193-29560	Sequence 29560, A
c	45	10	1.9	2381	9 US-09-880-107-3353	Sequence 3453, App
c	46	10	1.9	238033	17 US-10-159-563-337	Sequence 337, App
c	47	10	1.9	237326	15 US-10-301-844-1	Sequence 2, Appli
c	48	10	1.9	237326	15 US-10-301-844-2	Sequence 2, Appli
c	49	10	1.9	684707	17 US-10-398-221-9	Sequence 9, Appli
c	50	10	1.9	301208	17 US-10-398-221-2058	Sequence 115614, App
c	51	9	1.7	408	20 US-10-425-115-15614	Sequence 501, App
c	52	9	1.7	699	18 US-10-333-184-501	Sequence 14823, A
c	53	9	1.7	709	21 US-10-487-901-2882	Sequence 158940, App
c	54	9	1.7	741	20 US-10-425-115-158940	Sequence 2122, App
c	55	9	1.7	764	21 US-10-487-901-6701	Sequence 2122, App
c	56	9	1.7	855	19 US-10-437-963-101872	Sequence 81448, A
c	57	9	1.7	951	17 US-10-369-493-12428	Sequence 42428, A
c	58	9	1.7	957	20 US-10-425-115-14823	Sequence 14823, A
c	59	9	1.7	1700	17 US-10-388-934-316	Sequence 21988, A
c	60	9	1.7	1700	18 US-10-152-319A-2122	Sequence 21988, A
c	61	9	1.7	1753	18 US-10-424-599-21988	Sequence 21988, A
c	62	9	1.7	3819	19 US-10-437-963-101678	Sequence 81678, A
c	63	9	1.7	6509	19 US-10-437-963-66978	Sequence 66978, A
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c 66	9	1.7	252907	20	US-10-417-375-66	Sequence 66, App1	Sequence 122, App
c 67	8	1.5	25	22	US-10-843-527-28893	Sequence 28893, A	Sequence 234, App
c 68	8	1.5	25	22	US-10-843-527-28895	Sequence 28895, A	Sequence 234, App
c 69	8	1.5	25	22	US-10-843-527-206854	Sequence 206854,	Sequence 234, App
c 70	8	1.5	25	20	US-10-843-527-20730	Sequence 20730,	Sequence 234, App
c 71	8	1.5	60	10	US-09-108-915-18851	Sequence 19851, A	Sequence 21496, A
c 72	8	1.5	215	20	US-10-425-115-103673	Sequence 103673,	Sequence 152669,
c 73	8	1.5	301	17	US-10-027-632-12400	Sequence 12420,	Sequence 152669,
c 74	8	1.5	301	17	US-10-027-632-12420	Sequence 12420,	Sequence 165402,
c 75	8	1.5	321	19	US-10-767-995-4558	Sequence 4558, App1	Sequence 165402,
c 76	8	1.5	345	19	US-10-437-963-28074	Sequence 28074, A	Sequence 165402,
c 77	8	1.5	369	19	US-10-437-963-100412	Sequence 100412,	Sequence 18204, A
c 78	8	1.5	372	9	US-09-164-761-195	Sequence 195, App1	Sequence 18204, A
c 79	8	1.5	390	21	US-10-461-862-49	Sequence 49, App1	Sequence 18204, A
c 80	8	1.5	395	9	US-09-833-790-207	Sequence 207, App1	Sequence 18204, A
c 81	8	1.5	429	9	US-09-960-352-2228	Sequence 2218, App1	Sequence 1898, App
c 82	8	1.5	438	9	US-09-960-352-9784	Sequence 9784, App1	Sequence 1898, App
c 83	8	1.5	473	17	US-10-242-525A-121-23	Sequence 42123, A	Sequence 18203, A
c 84	8	1.5	473	18	US-10-085-873A-421-23	Sequence 42123, A	Sequence 18203, A
c 85	8	1.5	474	20	US-10-425-115-118288	Sequence 118288,	Sequence 18203, A
c 86	8	1.5	490	20	US-10-125-115-37022	Sequence 37022, A	Sequence 18203, A
c 87	8	1.5	511	20	US-10-363-145-69	Sequence 14569, A	Sequence 18203, A
c 88	8	1.5	511	20	US-10-362-345A-145-70	Sequence 14569, A	Sequence 18203, A
c 89	8	1.5	511	21	US-10-363-183A-145-69	Sequence 14569, A	Sequence 18203, A
c 90	8	1.5	511	21	US-10-363-145-70	Sequence 14570, A	Sequence 18203, A
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c 93	8	1.5	524	19	US-10-363-145-69	Sequence 14569, A	Sequence 18203, A
c 94	8	1.5	526	13	US-10-027-632-276920	Sequence 276920,	Sequence 18203, A
c 95	8	1.5	526	19	US-10-027-632-276920	Sequence 276920,	Sequence 18203, A
c 96	8	1.5	530	13	US-10-027-632-280289	Sequence 280289,	Sequence 18203, A
c 97	8	1.5	530	13	US-10-027-632-280289	Sequence 280289,	Sequence 18203, A
c 98	8	1.5	536	22	US-10-499-731-97	Sequence 97, App1	Sequence 18203, A
c 99	8	1.5	541	13	US-10-027-632-13184	Sequence 13184, A	Sequence 18203, A
c 100	8	1.5	541	13	US-10-027-632-13184	Sequence 13184, A	Sequence 18203, A
c 101	8	1.5	554	9	US-09-854-761-9014	Sequence 9014, App1	Sequence 18203, A
c 102	8	1.5	557	20	US-10-425-115-106414	Sequence 10614,	Sequence 18203, A
c 103	8	1.5	558	9	US-09-864-761-8151	Sequence 8151, App1	Sequence 18203, A
c 104	8	1.5	564	19	US-10-437-963-51869	Sequence 51869, A	Sequence 18203, A
c 105	8	1.5	578	13	US-10-027-632-105536	Sequence 105536,	Sequence 18203, A
c 106	8	1.5	578	13	US-10-027-632-289806	Sequence 289806,	Sequence 18203, A
c 107	8	1.5	578	17	US-10-027-632-10536	Sequence 105536,	Sequence 18203, A
c 108	8	1.5	578	17	US-10-027-632-289806	Sequence 289806,	Sequence 18203, A
c 109	8	1.5	585	13	US-10-027-632-195227	Sequence 195227,	Sequence 18203, A
c 110	8	1.5	585	17	US-10-027-632-195227	Sequence 195227,	Sequence 18203, A
c 111	8	1.5	587	9	US-09-761-13534	Sequence 13594, A	Sequence 18203, A
c 112	8	1.5	612	18	US-10-425-114-18884	Sequence 19884, A	Sequence 18203, A
c 113	8	1.5	633	20	US-10-363-345A-33829	Sequence 33829, A	Sequence 18203, A
c 114	8	1.5	633	20	US-10-363-345A-33829	Sequence 33830, A	Sequence 18203, A
c 115	8	1.5	644	17	US-10-027-632-284650	Sequence 284650,	Sequence 18203, A
c 116	8	1.5	633	21	US-10-363-483A-33829	Sequence 33830, A	Sequence 18203, A
c 117	8	1.5	644	17	US-10-027-632-284650	Sequence 284650,	Sequence 18203, A
c 118	8	1.5	644	13	US-10-027-632-284651	Sequence 284651,	Sequence 18203, A
c 119	8	1.5	644	13	US-10-027-632-284652	Sequence 284652,	Sequence 18203, A
c 120	8	1.5	644	17	US-10-027-632-284650	Sequence 284650,	Sequence 18203, A
c 121	8	1.5	644	17	US-10-027-632-284651	Sequence 284651,	Sequence 18203, A
c 122	8	1.5	644	17	US-10-027-632-284652	Sequence 284652,	Sequence 18203, A
c 123	8	1.5	644	19	US-10-027-963-4766	Sequence 47666, A	Sequence 18203, A
c 124	8	1.5	650	20	US-10-425-115-21496	Sequence 155889,	Sequence 18203, A
c 125	8	1.5	666	17	US-10-363-145-15889	Sequence 155889,	Sequence 18203, A
c 126	8	1.5	746	13	US-10-027-632-16338	Sequence 16338,	Sequence 18203, A
c 127	8	1.5	686	17	US-10-027-632-16938	Sequence 16938,	Sequence 18203, A
c 128	8	1.5	692	20	US-10-025-115-101692	Sequence 101692,	Sequence 18203, A
c 129	8	1.5	705	17	US-10-022-122A-20195	Sequence 20195, A	Sequence 18203, A
c 130	8	1.5	706	19	US-10-027-701-3505	Sequence 3505, App1	Sequence 18203, A
c 131	8	1.5	729	17	US-10-282-122A-13612	Sequence 13612,	Sequence 18203, A
c 132	8	1.5	746	13	US-10-027-632-150370	Sequence 150370,	Sequence 18203, A
c 133	8	1.5	746	20	US-10-027-632-165402	Sequence 165402,	Sequence 18203, A
c 134	8	1.5	746	20	US-10-027-632-165402	Sequence 165402,	Sequence 18203, A
c 135	8	1.5	747	17	US-10-369-433-37790	Sequence 37790, A	Sequence 18203, A
c 136	8	1.5	747	18	US-10-424-114-15828	Sequence 103353,	Sequence 18203, A
c 137	8	1.5	760	9	US-09-731-872-122	Sequence 122, App1	Sequence 18203, A
c 138	8	1.5	760	10	US-09-876-997-122	Sequence 122, App1	Sequence 18203, A

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 9, 2005, 17:15:15 ; Search time 253.703 Seconds

(without alignments)  
 3456.970 Million cell updates/sec

Title: US-09-776-865-2  
 Perfect score: 536  
 Sequence: 1 MAAGAMTPRPVQPARPGGF.....LPAKGEVNWLNDHGHGRH 536

Scoring table: OLI GO

Xgapop 60.0 Xgapext 60.0  
 Ygapop 60.0 Ygapext 60.0  
 Fgapop 6.0 Fgapext 7.0  
 Delop 6.0 Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Word size: 1

Total number of hits satisfying chosen parameters:

2400006

Post-processing: Listing first 1000 summaries

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Command line parameters:

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-DB=Issued_Patents_NA -QFM=FastaP -SUFIXX=oligo -tni -MINMATCH=0.1 -LOOPCPU=0
-LOOPEXT=0 -UNITS_Bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40_cdi
-LISH=1000 -DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=G
-OUTEXT=pco -HEAPSIZE=500 -NMINLEN=0 -MAXLEN=500000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	536	100.0	2930	4	US-09-359-167-7	Sequence 7, Appli
2	529	98.7	2513	4	US-09-349-016-1834	Sequence 1, Appli
3	514	95.5	2602	4	US-09-359-167-1	Sequence 1, Appli
4	119	22.2	1229	4	US-09-023-655-660	Sequence 66, Appli
5	78	14.6	63783	4	US-09-349-016-13376	Sequence 13576, Appli
6	69	12.9	217	4	US-09-016-434-602	Sequence 602, Appli
7	61	11.4	1485	4	US-09-359-167-9	Sequence 9, Appli
8	61	11.4	2844	4	US-09-359-167-3	Sequence 3, Appli
9	45	8.4	601	4	US-09-349-016-63336	Sequence 63336, Appli
10	30	5.6	601	4	US-09-349-016-63313	Sequence 63333, Appli
11	30	5.6	601	4	US-09-349-016-63314	Sequence 63334, Appli
12	30	5.6	1485	4	US-09-359-167-11	Sequence 11, Appli

86	5	PCT-US96-05792-1	Sequence 1, Appli	c 159	8	1.5 254778 4	US-09-949-016-12417
87	5	PCT-US96-05792-3	Sequence 3, Appli	c 160	8	1.5 264206 4	US-09-949-016-12731
88	8	US-09-539-33D-170	Sequence 170, App	c 161	8	1.5 264304 4	US-09-949-016-12409
89	8	US-09-552-991A-9569	Sequence 9569, AP	c 162	8	1.5 275110 4	US-09-949-016-12706
90	8	US-09-710-279-4211	Sequence 4211, AP	c 163	8	1.5 275110 4	US-09-949-016-16076
c 91	8	US-09-710-279-4211	Sequence 4202, AP	c 164	8	1.5 41924 4	US-09-949-016-12896
c 92	8	US-09-792-024-62	Sequence 62, Appli	c 165	8	1.5 451925 4	US-09-949-016-17305
c 93	8	US-09-792-024-58	Sequence 58, Appli	c 166	8	1.5 1664976 4	US-09-949-016-41211
c 94	8	US-09-792-024-58	Sequence 3372, AP	c 167	8	1.5 1664976 4	US-09-949-016-41211
95	8	US-09-710-279-3372	Sequence 5402, AP	c 168	8	1.5 4403765 3	US-09-103-840A-2
96	8	US-09-920-540-933	Sequence 933, App	c 169	8	1.5 4411529 3	US-09-866-108A-4132
97	8	US-09-949-016-13135	Sequence 13135, A	c 170	7	1.3 25	US-09-866-108A-4133
c 98	8	US-09-949-016-16706	Sequence 16706, A	c 171	7	1.3 25	US-09-866-108A-4133
c 99	8	US-09-949-016-16706	Sequence 976, App	c 172	7	1.3 25	US-09-866-108A-4134
c 100	8	US-09-949-016-16759	Sequence 16359, A	c 173	7	1.3 25	US-09-866-108A-4135
101	8	US-09-949-016-17225	Sequence 17225, A	c 174	7	1.3 25	US-09-866-108A-4136
102	8	US-09-920-540-1151	Sequence 1151, AP	c 175	7	1.3 25	US-09-866-108A-4137
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105	8	US-09-949-016-15750	Sequence 15750, A	c 178	7	1.3 25	US-09-866-108A-4139
106	8	US-09-976-976-7	Sequence 7, Appli	c 179	7	1.3 37	US-09-120-561C-4
107	8	US-09-909-547-7	Sequence 7, Appli	c 180	7	1.3 66	US-09-513-999C-16232
c 108	8	US-09-566-852B-4	Sequence 1, Appli	c 181	7	1.3 67	US-09-24-690A-56
c 109	8	US-09-902-540-1209	Sequence 1209, AP	c 182	7	1.3 67	US-09-908-555-56
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c 111	8	US-09-902-540-1211	Sequence 1211, AP	c 184	7	1.3 110	US-08-482-073-2
c 112	8	US-09-949-016-15030	Sequence 15030, A	c 185	7	1.3 131	US-09-621-076-17442
c 113	8	US-09-902-540-1221	Sequence 1221, AP	c 186	7	1.3 137	US-09-513-294A-6414
c 114	8	US-09-949-016-12487	Sequence 12487, A	c 187	7	1.3 140	US-09-621-076-17457
c 115	8	US-09-902-540-12624	Sequence 12622, AP	c 188	7	1.3 148	US-09-270-167-2675
c 116	8	US-09-949-016-12111	Sequence 11873, A	c 189	7	1.3 167	US-09-513-999C-33418
c 117	8	US-09-949-016-16460	Sequence 16460, A	c 190	7	1.3 185	US-09-270-167-28795
c 118	8	US-09-949-016-13363	Sequence 13363, A	c 191	7	1.3 185	US-09-270-167-2422
c 119	8	US-09-949-016-13576	Sequence 13576, A	c 192	7	1.3 185	US-09-313-294A-6414
c 120	8	US-09-740-041-3	Sequence 3, Appli	c 193	7	1.3 189	US-09-107-532A-2866
c 121	8	US-09-949-016-12508	Sequence 12608, A	c 194	7	1.3 190	US-09-513-999C-8555
c 122	8	US-09-949-016-16356	Sequence 16356, A	c 195	7	1.3 207	US-09-270-167-3037
c 123	8	US-09-949-016-11873	Sequence 12345, A	c 196	7	1.3 208	US-09-621-076-884
c 124	8	US-09-949-016-12245	Sequence 15758, A	c 197	7	1.3 213	US-09-189-060B-894
c 125	8	US-09-949-016-13363	Sequence 13783, A	c 198	7	1.3 213	US-09-902-40-8561
c 126	8	US-09-949-016-13576	Sequence 17150, A	c 199	7	1.3 214	US-09-242-690A-10
c 127	8	US-09-949-016-12160	Sequence 16320, A	c 200	7	1.3 214	US-09-908-855-10
c 128	8	US-09-949-016-17268	Sequence 12160, A	c 201	7	1.3 217	Patent No. 5217870
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c 131	8	US-09-949-016-17150	Sequence 16320, A	c 204	7	1.3 222	Sequence 11411, A
c 132	8	US-09-949-016-16320	Sequence 10347, A	c 205	7	1.3 225	Sequence 12859, A
c 133	8	US-09-949-016-12160	Sequence 119032, A	c 206	7	1.3 228	Sequence 2469, Ap
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c 141	8	US-09-949-016-14884	Sequence 14884, A	c 214	7	1.3 256	Sequence 21, Appli
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c 144	8	US-09-949-016-12881	Sequence 14881, A	c 223	7	1.3 279	Sequence 9776, Ap
c 145	8	US-09-949-016-14376	Sequence 14376, A	c 218	7	1.3 263	Sequence 27104, A
c 146	8	US-09-949-016-15425	Sequence 14519, A	c 219	7	1.3 265	Sequence 5500, Ap
c 147	8	US-09-949-016-12835	Sequence 12835, A	c 220	7	1.3 266	Sequence 532, App
c 148	8	US-09-949-016-12836	Sequence 12836, A	c 221	7	1.3 266	Sequence 975, App
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c 150	8	US-09-949-016-14517	Sequence 14516, A	c 223	7	1.3 279	Sequence 16, Appli
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c 152	8	US-09-949-016-14519	Sequence 14518, A	c 225	7	1.3 291	Sequence 17226, A
c 153	8	US-09-949-016-12569	Sequence 14445, A	c 226	7	1.3 297	US-09-107-433-512
c 154	8	US-09-949-016-14445	Sequence 14445, A	c 227	7	1.3 302	US-09-16-434-915
c 155	8	US-09-949-016-17227	Sequence 17227, A	c 228	7	1.3 309	US-09-710-279-291
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c 157	8	US-09-949-016-13527	Sequence 17229, A	c 230	7	1.3 310	US-09-936-941-16
c 158	8	US-09-949-016-17227	Sequence 17227, A	c 231	7	1.3 324	US-09-240-274-122



c 79	9	1.7	715	10	ADC75987	DNA homolog	152	8	1.5	ABQ47238
c 80	9	1.7	764	10	ADK17608	DNA (seq)	153	8	1.5	ABD310820
c 81	9	1.7	764	10	ADK59318	Plant DNA	154	8	1.5	AD55268
c 82	9	1.7	764	11	ADM45659	Adm5659	155	8	1.5	Aca32325
c 83	9	1.7	951	13	ADT43990	Insect re	c 156	8	1.5	Aah88245
c 84	9	1.7	1373	10	AAN80941	Bacterial	c 157	8	1.5	AHAH88445
c 85	9	1.7	1700	10	ADB59088	Aan80941	c 158	8	1.5	Aca25742
c 86	9	1.7	1700	10	ADB53647	Toxicity-	c 159	8	1.5	AdS62116
c 87	9	1.7	1700	10	ABT42420	Primarity	c 160	8	1.5	AHH64946
c 88	9	1.7	1700	12	ADP72853	Toxicity	c 161	8	1.5	Aah64958
c 89	9	1.7	2031	4	AB126653	Renal tox	c 162	8	1.5	Abd00520
c 90	9	1.7	2316	10	ADB59023	Drosophil	c 163	8	1.5	Klebsiell
c 91	9	1.7	2702	4	ABL25006	Toxicity-	c 164	8	1.5	Aaf22331
c 92	9	1.7	6028	4	ABL03360	Drosophil	c 165	8	1.5	Human sec
c 93	9	1.7	7125	4	ABL26652	Drosophil	c 166	8	1.5	Abq31613
c 94	9	1.7	51961	10	ADC20666	Human sec	c 167	8	1.5	Abq31612
c 95	9	1.7	51961	10	ABT16905	Human sec	c 168	8	1.5	Pseudomon
c 96	9	1.7	51961	10	ABZ67488	Human sec	c 169	8	1.5	Aai67947
c 97	9	1.7	247544	12	ADO59419	Human can	c 170	8	1.5	Oligonucle
c 98	9	1.7	252907	13	ADB32654	Human can	c 171	8	1.5	Abq31613
c 99	8	1.5	60	6	ABR47103	Human spl	c 172	8	1.5	AAK83808
c 100	8	1.5	144	6	ABO90618	M. capsul	c 173	8	1.5	Human imm
c 101	8	1.5	168	13	ADS04142	Human imm	c 174	8	1.5	AAK71739
c 102	8	1.5	289	5	ABA14613	Staphyloc	c 175	8	1.5	AAC77321
c 103	8	1.5	318	2	AAT07025	Human ner	c 176	8	1.5	AAC76669
c 104	8	1.5	321	13	ADR3777	Cotton cd	c 177	8	1.5	AAK83808
c 105	8	1.5	330	11	ADB04894	Pseudomon	c 178	8	1.5	AAK83755
c 106	8	1.5	331	4	AAK90500	Human dig	c 179	8	1.5	Aspergill
c 107	8	1.5	341	5	ABA11025	Human ner	c 180	8	1.5	Aah32620
c 108	8	1.5	365	5	ABA11025	Human ner	c 181	8	1.5	S. epider
c 109	8	1.5	372	4	AAI10274	Probe #20	c 182	8	1.5	Aad1110
c 110	8	1.5	372	4	ABA51911	Human foe	c 183	8	1.5	Abx76387
c 111	8	1.5	372	4	AAI31521	Probe #20	c 184	8	1.5	Lung canc
c 112	8	1.5	372	4	ABA21729	Probe #19	c 185	8	1.5	Abx76303
c 113	8	1.5	372	4	Aak56416	Human bon	c 186	8	1.5	Abx76387
c 114	8	1.5	372	4	Aak05206	Human bra	c 187	8	1.5	Human sma
c 115	8	1.5	372	4	AB525225	Human liv	c 188	8	1.5	Abx76387
c 116	8	1.5	372	4	AAI0211	Probe #20	c 189	8	1.5	Abx76303
c 117	8	1.5	372	6	ABs00217	Human gen	c 190	8	1.5	AAV41733
c 118	8	1.5	383	10	Add33833	Mouse mit	c 191	8	1.5	Ado02848
c 119	8	1.5	385	11	ABN1111	Human ORF	c 192	8	1.5	Abd0216
c 120	8	1.5	390	13	ABD32839	Human can	c 193	8	1.5	Abx76387
c 121	8	1.5	395	6	AA561666	Lung smal	c 194	8	1.5	Abx76387
c 122	8	1.5	395	6	AB525225	Bovine ES	c 195	8	1.5	ADBB8216
c 123	8	1.5	429	8	ABX37053	Bovine ES	c 196	8	1.5	AAK52844
c 124	8	1.5	430	4	AAI90901	Human pol	c 197	8	1.5	Abx76387
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c 127	8	1.5	499	10	ADF61849	Human aid	c 200	8	1.5	Abd06553
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c 130	8	1.5	552	12	ADQ92266	Human cDN	c 203	8	1.5	Abd11075
c 131	8	1.5	554	4	AAI18343	Human aut	c 204	8	1.5	Aak53737
c 132	8	1.5	554	4	AAI18344	Probe #82	c 205	8	1.5	Abd04421
c 133	8	1.5	554	4	ABA63344	Human foe	c 206	8	1.5	Aab63340
c 134	8	1.5	554	4	AAI43458	Probe #12	c 207	8	1.5	Abi18113
c 135	8	1.5	554	4	ABA30548	Probe #90	c 208	8	1.5	Abi52216
c 136	8	1.5	554	4	AAK37586	Human foe	c 209	8	1.5	Abi52276
c 137	8	1.5	554	4	Aak11885	Human bra	c 210	8	1.5	Abi52651
c 138	8	1.5	554	4	AB537247	Human liv	c 211	8	1.5	Abi52837
c 139	8	1.5	554	6	AB511572	Human gen	c 212	8	1.5	Abi52352
c 140	8	1.5	554	4	AAI17420	Probe #73	c 213	8	1.5	Abi5240
c 141	8	1.5	554	4	ABA62344	Human foe	c 214	8	1.5	Abi52447
c 142	8	1.5	558	4	AAI42322	Probe #11	c 215	8	1.5	Abi527080
c 143	8	1.5	558	4	ABA29685	Probe #81	c 216	8	1.5	Abi53071
c 144	8	1.5	558	4	AAK36564	Human bra	c 217	8	1.5	Abi53507
c 145	8	1.5	558	4	AAK10678	Human bra	c 218	8	1.5	Abi53507
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c 148	8	1.5	566	5	AAS9259	DNA encod	c 221	8	1.5	Abi53507
c 149	8	1.5	587	4	AAC37568	Human bra	c 222	8	1.5	Abi53507
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 9, 2005, 13:42:45 ; Search time 6823.47 Seconds

(without alignments)  
3806.273 Million cell updates/sec

Title: US-09-776-865-2  
Perfect score: 536  
Sequence: 1 MAAGAMTPRPPQPARPGF.....LPAKGEVQNWAINDHHGHRH 536

Scoring table: OJIGO

Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9408497

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing First 1000 summaries

DB parameters:  
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Database : GenBank : \*

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4	529	98.7	2512	9	AJ387747	Homo sapi
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					BC020961	Homo sapi
					CQ77623	Sequence
					BD248125	GBS toxin
					CQ783928	Sequence
					BD127905	Primer fo
					AK075320	Homo sapi
					CQ782221	Sequence
					BD126330	Primer fo
					CQ780684	Sequence
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					AF244578	Ovis aries
					BD248126	GBS toxin
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					AL590427	Human DNA
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c	79	11	2.1	143036	9	AC040936	Homo sapi	AC101499	Mus muscu
c	80	11	2.1	146779	2	AC119499	Rattus no	AC003345	Drosophil
c	81	11	2.1	146515	9	AC040099	Homo sapi	AC027032	Arabidops
c	82	11	2.1	201957	2	AC113306	Mus muscu	AC024226	Genomic S
c	83	11	2.1	215541	2	AC016904	Homo sapi	AC079334	Homo sapi
c	84	11	2.1	243850	2	AC114710	Rattus no	BX276180	Zebrafish
c	85	11	2.1	323443	2	AC145086	Mus muscu	AC104084	Homo sapi
c	86	10	1.9	448	9	F36248950	Homo sapi	AC120336	Continuation (2 of
c	87	10	1.9	657	6	AX415590	Sequence	AC110000	Continuation (9 of
c	88	10	1.9	1874	10	BC018306	Mus muscu	AP006501	Continuation (10 o
c	89	10	1.9	2266	6	AR036570	Sequence	AP006501_09	Continuation (10 o
c	90	10	1.9	2266	6	BD084119	Polymorph	AC018326	Drosophil
c	91	10	1.9	2270	6	CET07A5	Caenorhabdi	AL049843	Human DNA
c	92	10	1.9	2281	6	AX410807	Sequence	AL031276	Human DNA
c	93	10	1.9	2281	9	HSU09544	Human sodiu	AP003812	Oryza sat
c	94	10	1.9	6359	8	YSCY164A	M88172	AC126564	Oryza sat
c	95	10	1.9	19371	3	CEK10G9	Saccharomy	AC112039	Oryza sat
c	96	10	1.9	2266	6	BD084119	Polymorph	AC1134048	Oryza sat
c	97	10	1.9	2270	6	CQ715838	Sequence	AC140867	Homo sapi
c	98	10	1.9	80091	9	AC094088	Homo sapi	AL928756	Oryza sat
c	99	10	1.9	83412	2	AC133611	Sequence	AL928859	Oryza sat
c	100	10	1.9	84707	6	AX417037	Rattus no	AL606617	Mouse DNA
c	101	10	1.9	136646	9	AL138726	Human DNA	AP003444	Oryza sat
c	102	10	1.9	148975	2	AC012145	Homo sapi	AC115852	Mus muscu
c	103	10	1.9	167098	2	AC023952	Homo sapi	AP003442	Oryza sat
c	104	10	1.9	178044	2	AC121663	Rattus no	AC140867	Homo sapi
c	105	10	1.9	183698	10	AL606464	Mouse DNA	AC074661	Homo sapi
c	106	10	1.9	186662	10	AL690388	Mouse DNA	AC074662	Rattus no
c	107	10	1.9	209816	2	AL627315	Mus muscu	AP00391	Oryza sat
c	108	10	1.9	209816	2	AL627315	Human DNA	AC018774	Homo sapi
c	109	10	1.9	235033	6	BD084121	Polymorph	AC018774	Oryza sat
c	110	10	1.9	237246	6	BD084122	Polymorph	AP005744	Oryza sat
c	111	10	1.9	240774	2	AC130391	Rattus no	AP006266	Oryza sat
c	112	10	1.9	246240	6	AR036572	Sequence	AC125085	Mus muscu
c	113	10	1.9	246240	6	AR036573	Sequence	AC11740	Rattus no
c	114	10	1.9	246240	6	AR036574	Sequence	AC093583	Drosophil
c	115	10	1.9	246282	9	HSU091328	Human lared	AL607143	Mouse DNA
c	116	10	1.9	305050	1	AL596173	Listeria	AC007467	Oryza sat
c	117	10	1.9	349980	6	AX417036	Sequence	AC007467	Drosophil
c	118	10	1.9	349980	6	AX417048	Sequence	AC007467	Human DNA
c	119	9	1.7	28	6	CQ778224	Sequence	AC011221	Homo sapi
c	120	9	1.7	464	10	G52591	SHGC-81575	AC120885	Ecdyse
c	121	9	1.7	495	11	F3616173	Mus muscu	AC139981	Rattus no
c	122	9	1.7	513	8	AF318651	Salolala z	AL611934	Mouse DNA
c	123	9	1.7	699	6	AX364494	Sequence	AC025334	Homo sapi
c	124	9	1.7	880	8	AY275580	Nevea bra	AC143322	Rattus no
c	125	9	1.7	960	5	CR733177	Gallus ga	AC126562	Rattus no
c	126	9	1.7	1432	10	AY102171	Rattus no	AC141592	Homo sapi
c	127	9	1.7	1684	10	BC018710	Rattus no	AC143324	Homo sapi
c	128	9	1.7	1700	6	AX827782	Sequence	AC126603	Homo sapi
c	129	9	1.7	1700	10	RNU28504	Rattus norv	AC142534	Homo sapi
c	130	9	1.7	1848	10	BC078748	Rattus no	AC142534	Rattus no
c	131	9	1.7	1885	10	MNPTICT	Sequence	AC132552	Rattus no
c	132	9	1.7	2004	10	BC013445	Mus muscu	AC134678	Homo sapi
c	133	9	1.7	2031	6	CO609462	Sequence	AC016770	Homo sapi
c	134	9	1.7	2229	10	AB025242	Rattus no	AC099028	Drosophil
c	135	9	1.7	2316	9	Q574523	Sequence	AC123325	Mus muscu
c	136	9	1.7	2700	14	AF238232	Bovine ad	AC143322	Homo sapi
c	137	9	1.7	2702	6	CO606992	Sequence	AC132552	Rattus no
c	138	9	1.7	3021	3	AY119484	Drosophil	AC134678	Homo sapi
c	139	9	1.7	5000	14	AF032994	Trichoplus	AC1470152	Mus muscu
c	140	9	1.7	5111	10	AF308433	Mus muscu	AC108431	Mus muscu
c	141	9	1.7	6028	6	Q609461	Sequence	AL606466	Mouse DNA
c	142	9	1.7	7125	6	MMU19755	Mus domesti	AC04411	Mus muscu
c	143	9	1.7	11172	10	AB01203	Treponema	AC011374	Homo sapi
c	144	9	1.7	1433	1	AJ320524	Mus muscu	AC011374	Mus muscu
c	145	9	1.7	26506	10	MMU320524	Mus muscu	AC011374	Mus muscu
c	146	9	1.7	43219	2	AC100163	Mus muscu	AC011374	Mus muscu
c	147	9	1.7	55197	2	AC120651	Rattus no	AC011374	Mus muscu
c	148	9	1.7	55197	2	AC017529	Drosophil	AC011374	Mus muscu
c	149	9	1.7	62172	9	AC140118	Homo sapi	AC011374	Mus muscu
c	150	9	1.7	62676	2	AC072047	Arabidops	AC122380	Mus muscu

Field	Value						
Gencore version	5.1.6						
Copyright (c) 1993 - 2005	Compugen Ltd.						
protein - nucleic search, using frame_plus_P2n model							
on:	July 9, 2005, 16:46:21 ; Search time 4589.43 Seconds (without alignment) 4105.478 Million cell updates/sec						
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ygapop	60.0 , Ygapext 60.0						
rgapop	6.0 , Rgapext 7.0						
delop	6.0 , Delext 7.0						
arched:	34239544 seqs, 19032134700 residues						
nd size:	1						
al number of hits satisfying chosen parameters:	68477535						
imum DB seq length: 0							
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it-processing: Listing first 1000 summaries							
mand line parameters:							
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-DBST=FASTA -QEXT=0 -FASTAP -SUSP09776865/runat_08072005_175612_23695/app_query.fasta_1.1358							
-BITS=bits -START=1 -BND=-1 -MATRIX=G_OIG0 -TRANS=human40.cdi -LIST=1000							
-CALIGN=C 200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODB=LOCAL -OUTFWT=pfo							
-CAGL=ext -HEAPS125000 MINLEN=200000000 MAXLEN=200000000							
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-N TIMEOUT=200 -WARN TIMEOUT=30 -THREADS=1 -XCAPOP=60 -XGAPEXT=60 -FGAPOP=6							
-YAPOP=60 -YGAPEXT=7 -YGAPEXT=60 -DELEXT=6 -DELEXT=7 -YGAPEXT=60 -YGAPEXT=7							
abase :	EST:*						
1: gb_est1:*							
2: gb_est2:*							
3: gb_ntc:*							
4: gb_est3:*							
5: gb_est4:*							
6: gb_est5:*							
7: gb_est6:*							
8: gb_gss1:*							
9: gb_gss2:*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
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No.							
1	168	33.9	721	7	CK833565	4057467	CK833565 4057467 B
2	168	33.9	737	7	CK833577	4057771	CK833577 4057771 B
3	162	32.7	700	7	CNT86597	4120614 B	CNT86597 4120614 B
4	94	19.0	758	6	CB166094	KX663014	CB166094 KX663014
5	64	12.9	947	7	C0579484	ILLOUNIGEN	C0579484 ILLOUNIGEN
6	61	12.3	432	1	AA258513	zr59d01_r	AA258513 zr59d01_r
7	61	12.3	537	6	CB158910	K-BEST0218	CB158910 K-BEST0218
8	61	12.3	537	6	CB158929	K-BEST0219	CB158929 K-BEST0219
9	61	12.3	570	5	CB158937	RPT245537	RPT245537 RPT245537

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84	23	4.6	731	7	CK696626	ZP101-P00	BJ060500
85	23	4.6	784	4.6	CK024678	AGENCOURT	CF289359
86	23	4.6	882	7	CN178455	AGENCOURT	BG907838
87	22	4.4	690	1	AJ447666	AJ447666	BQ737435
88	22	4.4	738	1	AJ455947	AJ455947	BF539146
89	22	4.4	810	1	AJ455169	AJ455169	60205009
90	21	4.2	465	5	BQ322417	RCS-CS002	CC295340
91	21	4.2	610	5	AL792191	AL792191	CH61-82B
92	21	4.2	772	2	BF123545	BF123545	BY179630
93	21	4.2	2674	3	AK014522	Mus muscu	CB757730
94	20	4.0	334	1	AJ734268	AJ734268	BY317931
95	20	4.0	445	2	BE3175421	BE3175421	AQ224962
96	20	4.0	587	9	CR035573	Forward_s	HS-200
97	20	4.0	589	5	BUI27798	BUI27798	BP44752
98	20	4.0	618	7	CF170114	B0822G02-	BP44752
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100	20	4.0	711	4	BIG97765	BD3346858	CB50518
101	20	4.0	730	6	CA327442	CA327442	BM804862
102	20	4.0	785	1	CP285351	CP285351	AGENCOURT
103	20	4.0	791	7	CV110899	CV110899	CD730551
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107	19	3.8	870	5	BO345391	MR4-NFT014	BF537689
108	19	3.8	931	5	BI190277	BI190277	602054577
109	18	3.6	311	5	BUI38011	BUI38011	AK050277
110	18	3.6	345	5	BY138011	BY138011	AK050184
111	18	3.6	349	6	BY793266	BY793266	AK040717
112	18	3.6	355	5	BY0118610	AGENCOURT	Mus muscu
113	18	3.6	423	5	BY274305	BY274305	CD730551
114	18	3.6	426	5	BY284055	BY284055	BP361755
115	18	3.6	427	5	BY278620	BY278620	BP361755
116	18	3.6	436	5	BY246932	BY246932	BP361755
117	18	3.6	440	5	BY031138	BY031138	BP309703
118	18	3.6	447	6	CB747168	CB747168	CB583897
119	18	3.6	457	5	BY241444	BY241444	AMGNNUC:C
120	18	3.6	471	5	BY245489	BY245489	BY247147
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122	18	3.6	482	6	CB728076	CB728076	BY723745
123	18	3.6	494	5	BY254429	BY254429	AL973749
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127	18	3.6	582	5	BP285070	BP285070	BU611275
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133	18	3.6	904	4	BF124137	BF124137	BU611275
134	18	3.6	965	4	BG290613	BG290613	BU611275
135	18	3.6	1100	4	CG635332	602785577	BU611275
136	17	3.4	1165	5	BQ715048	AGENCOURT	CF289359
137	16	3.2	425	6	CK688160	ZF101-P00	CF289359
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139	16	3.2	412	6	BY645660	BY645660	CF289359
140	16	3.2	423	9	CG635332	OST4.9032	CF289359
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142	16	3.2	495	6	CB713294	AMGNNUC:C	CF289359
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152	14	2.8	630	2	BB610013	BB610013	CF289359
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14	2.8	175	12	CP285351	CP285351	CP285351	CP285351
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14	2.8	178	11	CP0118610	AGENCOURT	CP0118610	AGENCOURT
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14	2.8	181	11	BI190277	BI190277	BI190277	BI190277
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14	2.8	183	11	BY793266	BY793266	BY793266	BY793266
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14	2.8	189	11	BY793266	BY793266	BY793266	BY793266
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14	2.8	209	11	CK688160	ZF101-P00	CK688160	ZF101-P00
14	2.8	210	11	CB700764	AMGNNUC:C	CB700764	AMGNNUC:C
14	2.8	211	11	CB693459	AMGNNUC:C	CB693459	AMGNNUC:C
14	2.8	212	11	BY645660	BY645660	BY645660	BY645660
14	2.8	213	10	CG635332	OST4.9032	CG635332	OST4.9032
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14	2.8	215	10	BY021590	BY021590	BY021590	BY021590
14	2.8	216	10	CB760265	CB760265	CB760265	CB760265
14	2.8	217	10	BI041275	MR4-NFT014	BI041	

GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 9, 2005, 21:49:36 ; Search time 840.204 Seconds  
 (without alignments)  
 36395.824 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 495

Sequence: 1 MKSFVSDLAPSDGEEGSDRT.....LPAKGEVNWAISDHQGRN 495

Scoring table: OLIGO

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Delop	6.0	Delext	7.0

Searched: 6330943 seqb, 3139157217 residues

Word size: 1

Total number of hits satisfying chosen parameters: 12650797

Post-processing: Listing first 1000 summaries

Command line parameters:

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-DB=Public_Applications_NA -QFMT=fasta -SUFFIX=_app.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=T=0 -UNITS=bits -START=1 -END=-1 -MATRIX=Oligo
-TRANS=human40.0.cdi -LIST=100 -DOALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFORMAT=psl -NORM=ext -HEADPSL=100 -MINLEN=0
-MAXLEN=2000000000 -USER=US09776865 -@CGN_1.1_1065 @runat_08072005_175614_23755
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 16: /cgn2\_6/picodata/2/pubpna/US10D\_PUBCOMB.seq;\*  
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	%	Query Match	Length	DB ID	Description	
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4	61	12.3	1488	13	US-10-098-841-322	Sequence 946, App	
5	61	12.3	1651	17	US-10-264-237-946	Sequence 302, App	
6	61	12.3	1872	17	US-10-264-049-302	Sequence 461, App	
7	61	12.3	1975	18	US-10-296-115-461	Sequence 461, App	
c	8	61	12.3	1975	18	US-10-296-115-461	Sequence 461, App
9	61	12.3	2602	21	US-10-823-506-1	Sequence 1, Appli	
10	61	12.3	2626	14	US-10-198-846-12482	Sequence 12482, A	
11	61	12.3	2930	9	US-09-778-855-1	Sequence 1, Appli	
12	61	12.3	2930	21	US-10-823-506-7	Sequence 7, Appli	
13	61	12.3	3292	21	US-10-887-553A-858	Sequence 858, App	
14	61	12.3	3299	19	US-10-755-889-587	Sequence 587, App	
15	61	12.3	3362	10	US-09-814-353-19097	Sequence 19097, A	
16	48	9.7	1229	18	US-10-641-643-660	Sequence 660, App	
17	33	6.7	217	17	US-10-305-720-602	Sequence 102, App	
18	30	6.1	1485	21	US-10-823-506-11	Sequence 11, Appli	
19	29	5.9	196	9	US-09-878-178-1320	Sequence 1320, App	
20	29	5.9	196	13	US-10-046-935-1320	Sequence 1320, App	
21	29	5.9	196	14	US-10-146-102-1320	Sequence 1320, App	
22	29	5.9	494	10	US-09-814-353-12829	Sequence 12829, A	
23	29	5.9	498	10	US-09-814-353-46	Sequence 644, App	
24	29	5.9	516	14	US-10-198-846-9093	Sequence 9093, App	
25	29	5.9	573	9	US-09-728-446-128	Sequence 1228, App	
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29	12	2.4	512	16	US-10-029-386-556	Sequence 556, App	
30	12	2.4	2281	9	US-09-880-107-353	Sequence 3453, App	
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36	11	2.2	3423	16	US-10-233-045-21	Sequence 21, Appli	
37	11	2.2	3946	20	US-10-734-731-9	Sequence 9, Appli	
38	11	2.2	3946	20	US-10-807-560-9	Sequence 9, Appli	
39	11	2.2	3946	21	US-10-887-553A-1016	Sequence 1016, App	
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44	10	2.0	875	17	US-10-369-593-59558	Sequence 29556, A	
45	10	2.0	1425	17	US-10-369-493-59560	Sequence 29556, A	
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c	57	9	1.8	855	19	US-10-437-963-101872	Sequence 101872, A
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c	64	9	1.8	1952	9	US-09-835-232-5	Sequence 5, Appli
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c	66	9	1.8	1974	US-10-425-114-29922	Sequence 29922, A	c 139	8	1.6	US-10-363-483A-33830
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c	68	9	1.8	11069	US-10-337-953-86268	Sequence 86268, A	c 141	8	1.6	US-10-437-963-0087
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c	103	8	1.6	366	US-09-998-598-2170	Sequence 2170, APP	c 176	8	1.6	US-10-027-632-081536
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c	117	8	1.6	536	US-10-493-731-97	Sequence 6741, APP	c 190	8	1.6	US-10-027-632-081550
c	118	8	1.6	545	US-09-164-761-8717	Sequence 8717, APP	c 191	8	1.6	US-10-027-632-081551
c	119	8	1.6	562	US-10-857-294-281	Sequence 294, APP	c 192	8	1.6	US-10-027-632-081552
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c	124	8	1.6	587	US-09-264-761-13594	Sequence 9332, APP	c 197	8	1.6	US-10-027-632-081557
c	125	8	1.6	594	US-10-363-345A-2559	Sequence 25859, A	c 198	8	1.6	US-10-027-632-081558
c	126	8	1.6	594	US-10-363-345A-25860	Sequence 25859, A	c 199	8	1.6	US-10-027-632-081559
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c	130	8	1.6	600	US-10-956-157-6741	Sequence 9332, APP	c 203	8	1.6	US-10-027-632-081563
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c	132	8	1.6	632	US-10-027-632-2188079	Sequence 2188079, APP	c 205	8	1.6	US-10-027-632-081565
c	133	8	1.6	632	US-10-027-632-2188080	Sequence 2188080, APP	c 206	8	1.6	US-10-027-632-081566
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 9, 2005, 17:15:15 ; Search time 234.297 Seconds

(without alignments)

3456.970 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 495

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Scoring table: OLIGO

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Ygapext 60.0 , Ygapext 60.0

Fgapext 6.0 , Fgapext 7.0

Delopt 6.0 , Delopt 7.0

Searched: 1202984 seqs, 818139359 residues

Word size: 1

Total number of hits satisfying chosen parameters: 24000006

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Listing first 1000 summaries

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-DB=Issued_Patents_NA -QMPCL=0 _MINMATCH=0 _LOOPCCL=0
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-LIST=1000 -DOCAALIGN=100 -THR SCORE=Quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
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-FGAPEXT=7 -YGAPOP=60 -DELEXT=7
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6: /cgn2_6/podata/1/ina/backfilesl.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	495	100.0	2844	4	US-09-359-167-3	Sequence 3, Appli	Sequence 3, Appli
2	61	12.3	1485	4	US-09-359-167-9	Sequence 9, Appli	Sequence 9, Appli
3	61	12.3	2513	4	US-09-359-016-1834	Sequence 1, Appli	Sequence 1, Appli
4	61	12.3	2602	4	US-09-359-167-1	Sequence 7, Appli	Sequence 7, Appli
5	61	12.3	2930	4	US-09-359-167-7	Sequence 660, Appli	Sequence 660, Appli
6	48	9.7	1229	4	US-09-02655-660	Sequence 13576, A	Sequence 13576, A
7	43	8.7	6783	4	US-09-016-13376	Sequence 602, Appli	Sequence 602, Appli
8	33	6.7	217	4	US-09-016-434-602	Sequence 11, Appli	Sequence 11, Appli
9	30	6.1	1485	4	US-09-359-167-1	Sequence 11, Appli	Sequence 11, Appli
10	26	5.3	601	4	US-09-016-63313	Sequence 63313, A	Sequence 63313, A
11	26	5.3	601	4	US-09-016-63314	Sequence 63314, A	Sequence 63314, A
12	16	3.2	601	4	US-09-949-016-63336	Sequence 63336, A	Sequence 63336, A

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c	90	8	1.6	1263	4	US-09-352-99A-13467	Sequence 13467, App	8	8	1.6	156698
c	91	8	1.6	1263	4	US-09-232-99A-13658	Sequence 13658, App	8	8	1.6	177251
c	92	8	1.6	1335	4	US-09-270-767-13448	Sequence 13448, App	8	8	1.6	275110
c	93	8	1.6	1353	4	US-09-902-540-4241	Sequence 4241, App	8	8	1.6	374159
c	94	8	1.6	1377	4	US-09-232-99A-14676	Sequence 13676, App	8	8	1.6	1664976
c	95	8	1.6	1384	1	US-07-507-538C-1	Sequence 1, Appli	8	1.6	1664976	4
c	96	8	1.6	1384	2	US-08-162-40-B-1	Sequence 1, Appli	8	1.6	1664976	4
c	97	8	1.6	1384	4	US-09-364-185-1	Sequence 1, Appli	8	1.6	1664976	4
c	98	8	1.6	1419	4	US-09-302-540-5186	Sequence 5186, App	8	1.6	170	7
c	99	8	1.6	1536	4	US-09-252-99A-11652	Sequence 11652, App	8	1.6	171	7
c	100	8	1.6	1761	4	US-09-232-99A-11704	Sequence 11704, App	8	1.6	172	7
c	101	8	1.6	1811	4	US-09-740-041-1	Sequence 1, Appli	8	1.6	173	7
c	102	8	1.6	1934	2	US-08-162-40-B-7	Sequence 1, Appli	8	1.6	174	7
c	103	8	1.6	2052	3	US-09-134-001C-2739	Sequence 2739, App	8	1.6	175	7
c	104	8	1.6	2178	4	US-09-270-767-14275	Sequence 14275, App	8	1.6	176	7
c	105	8	1.6	2296	4	US-09-949-016-1182	Sequence 1182, App	8	1.6	177	7
c	106	8	1.6	2301	4	US-09-774-528-110	Sequence 110, App	8	1.6	178	7
c	107	8	1.6	2366	4	US-09-349-016-5483	Sequence 5483, App	8	1.6	179	7
c	108	8	1.6	2607	4	US-09-915-181A-1	Sequence 1, Appli	8	1.6	180	7
c	109	8	1.6	2626	4	US-09-949-016-745	Sequence 745, App	8	1.6	181	7
c	110	8	1.6	2703	4	US-09-248-756A-4178	Sequence 4178, App	8	1.6	182	7
c	111	8	1.6	2716	1	US-08-647-484-1	Sequence 1, Appli	8	1.6	183	7
c	112	8	1.6	2716	1	US-08-647-484-3	Sequence 3, Appli	8	1.6	184	7
c	113	8	1.6	2716	1	US-08-647-481-1	Sequence 1, Appli	8	1.6	185	7
c	114	8	1.6	2716	1	US-08-647-481-3	Sequence 3, Appli	8	1.6	186	7
c	115	8	1.6	2716	1	US-08-30-033A-1	Sequence 1, Appli	8	1.6	187	7
c	116	8	1.6	2716	1	US-08-30-033A-3	Sequence 3, Appli	8	1.6	188	7
c	117	8	1.6	2716	5	PCT-US96-05192-1	Sequence 1, Appli	8	1.6	189	7
c	118	8	1.6	2716	5	PCT-US96-05192-3	Sequence 3, Appli	8	1.6	190	7
c	119	8	1.6	2785	4	US-09-949-016-2651	Sequence 2651, App	8	1.6	191	7
c	120	8	1.6	2795	4	US-09-949-016-1115	Sequence 1135, App	8	1.6	192	7
c	121	8	1.6	2831	2	US-08-306-713-1	Sequence 1, Appli	8	1.6	193	7
c	122	8	1.6	3051	4	US-09-270-767-12928	Sequence 12928, App	8	1.6	194	7
c	123	8	1.6	3211	4	US-09-71-259-4211	Sequence 4211, App	8	1.6	195	7
c	124	8	1.6	3254	4	US-09-10-219-4202	Sequence 4202, App	8	1.6	196	7
c	125	8	1.6	3293	4	US-09-792-024-62	Sequence 62, Appli	8	1.6	197	7
c	126	8	1.6	3294	4	US-09-795-024-58	Sequence 1135, App	8	1.6	198	7
c	127	8	1.6	3563	4	US-09-710-219-3372	Sequence 3372, App	8	1.6	199	7
c	128	8	1.6	6468	4	US-09-302-540-895	Sequence 895, App	8	1.6	200	7
c	129	8	1.6	8205	4	US-09-949-016-1500	Sequence 1500, App	8	1.6	201	7
c	130	8	1.6	8220	4	US-09-949-016-932	Sequence 932, App	8	1.6	202	7
c	131	8	1.6	9377	4	US-09-301-874-3	Sequence 3, Appli	8	1.6	203	7
c	132	8	1.6	11854	4	US-09-902-540-1037	Sequence 1037, App	8	1.6	204	7
c	133	8	1.6	1287	4	US-09-949-016-16359	Sequence 16359, App	8	1.6	205	7
c	134	8	1.6	1297	4	US-09-949-016-13123	Sequence 13123, App	8	1.6	206	7
c	135	8	1.6	15543	4	US-09-949-016-17225	Sequence 17225, App	8	1.6	207	7
c	136	8	1.6	18000	4	US-09-949-016-1224	Sequence 17, Appli	8	1.6	208	7
c	137	8	1.6	19161	4	US-09-949-016-15731	Sequence 15731, A	8	1.6	209	7
c	138	8	1.6	20444	4	US-09-949-016-15750	Sequence 15750, A	8	1.6	210	7
c	139	8	1.6	20566	4	US-09-776-916-7	Sequence 7, Appli	8	1.6	211	7
c	140	8	1.6	20966	4	US-09-309-541-7	Sequence 1, Appli	8	1.6	212	7
c	141	8	1.6	216	4	US-09-569-852B-1	Sequence 12487, A	8	1.6	213	7
c	142	8	1.6	2201	4	US-09-657-316A-17	Sequence 12924, A	8	1.6	214	7
c	143	8	1.6	2791	4	US-09-540-1211	Sequence 1211, Ap	8	1.6	215	7
c	144	8	1.6	27180	4	US-09-949-016-16081	Sequence 12877, A	8	1.6	216	7
c	145	8	1.6	27383	4	US-09-949-016-14393	Sequence 14393, A	8	1.6	217	7
c	146	8	1.6	66504	4	US-09-740-041-3	Sequence 3, Appli	8	1.6	218	7
c	147	8	1.6	29465	4	US-09-949-016-12487	Sequence 12487, A	8	1.6	219	7
c	148	8	1.6	32573	4	US-09-949-016-13359	Sequence 13359, A	8	1.6	220	7
c	149	8	1.6	33885	4	US-09-949-016-16081	Sequence 16081, A	8	1.6	221	7
c	150	8	1.6	43255	4	US-09-949-016-11909	Sequence 11909, A	8	1.6	222	7
c	151	8	1.6	47799	4	US-09-949-016-13163	Sequence 13363, A	8	1.6	223	7
c	152	8	1.6	66504	4	US-09-949-016-13076	Sequence 13076, A	8	1.6	224	7
c	153	8	1.6	81819	4	US-09-949-016-16661	Sequence 16661, A	8	1.6	225	7
c	154	8	1.6	86119	4	US-09-949-016-16662	Sequence 16662, A	8	1.6	226	7
c	155	8	1.6	86114	4	US-09-949-016-12454	Sequence 12345, A	8	1.6	227	7
c	156	8	1.6	86114	4	US-09-949-016-15758	Sequence 15758, A	8	1.6	228	7
c	157	8	1.6	102008	4	US-09-949-016-16617	Sequence 16617, A	8	1.6	229	7
c	158	8	1.6	116966	4	US-09-949-016-17557	Sequence 17557, A	8	1.6	230	7